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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=2; day=17; hr=17; min=55; sec=43; ms=415; ]

=====

Output Set:

```

Started:      2009-01-28 11:51:44.120
Finished:    2009-01-28 11:52:12.303
Elapsed:     0 hr(s) 0 min(s) 28 sec(s) 183 ms
Total Warnings: 94
Total Errors:  498
No. of SeqIDs Defined: 401
Actual SeqID Count: 401

```

[illegible]

**Input Set:**

**Output Set:**

**Started:** 2009-01-28 11:51:44.120  
**Finished:** 2009-01-28 11:52:12.303  
**Elapsed:** 0 hr(s) 0 min(s) 28 sec(s) 183 ms  
**Total Warnings:** 94  
**Total Errors:** 498  
**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (37)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (37)
E 300	Invalid codon found Ala SEQID (37) POS: 577
E 300	Invalid codon found Cys SEQID (37) POS: 580
E 300	Invalid codon found Ser SEQID (37) POS: 583
E 300	Invalid codon found Ile SEQID (37) POS: 586
E 300	Invalid codon found Leu SEQID (37) POS: 589
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)

**Input Set:**

**Output Set:**

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**Total Warnings:** 94  
**Total Errors:** 498  
**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (61)
E 300	Invalid codon found Ala SEQID (61) POS: 149
E 300	Invalid codon found Asn SEQID (61) POS: 152
E 300	Invalid codon found Val SEQID (61) POS: 155
E 300	Invalid codon found Val SEQID (61) POS: 158
E 300	Invalid codon found Val SEQID (61) POS: 161
E 300	Invalid codon found Asp SEQID (61) POS: 164

**Input Set:**

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**Total Warnings:** 94  
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**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
E 300	Invalid codon found Gly SEQID (61) POS: 167
E 300	Invalid codon found Asn SEQID (61) POS: 170
E 300	Invalid codon found Thr SEQID (61) POS: 173
E 300	Invalid codon found Val SEQID (61) POS: 176
E 300	Invalid codon found Asn SEQID (61) POS: 179
E 300	Invalid codon found Leu SEQID (61) POS: 182
E 300	Invalid codon found Gly SEQID (61) POS: 185
E 300	Invalid codon found Leu SEQID (61) POS: 188
E 300	Invalid codon found Trp SEQID (61) POS: 191 This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (74)
W 402	Undefined organism found in <213> in SEQ ID (77)
W 402	Undefined organism found in <213> in SEQ ID (78)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (83)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (84)
W 402	Undefined organism found in <213> in SEQ ID (85)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (85)
W 402	Undefined organism found in <213> in SEQ ID (86)
E 355	Empty lines found between the amino acid numbering and the

**Input Set:**

**Output Set:**

**Started:** 2009-01-28 11:51:44.120  
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**Total Warnings:** 94  
**Total Errors:** 498  
**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (86)
W 402	Undefined organism found in <213> in SEQ ID (89)
W 402	Undefined organism found in <213> in SEQ ID (90)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (94)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (96)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (97)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (98)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (99)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (100)
W 402	Undefined organism found in <213> in SEQ ID (105)
W 402	Undefined organism found in <213> in SEQ ID (106)
W 402	Undefined organism found in <213> in SEQ ID (107)
W 402	Undefined organism found in <213> in SEQ ID (108)
W 402	Undefined organism found in <213> in SEQ ID (109)
W 402	Undefined organism found in <213> in SEQ ID (110)
W 402	Undefined organism found in <213> in SEQ ID (121)

**Input Set:**

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**Total Warnings:** 94  
**Total Errors:** 498  
**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (122)
W 402	Undefined organism found in <213> in SEQ ID (123)
W 402	Undefined organism found in <213> in SEQ ID (124)
W 402	Undefined organism found in <213> in SEQ ID (125)
W 402	Undefined organism found in <213> in SEQ ID (126)
W 402	Undefined organism found in <213> in SEQ ID (127)
W 402	Undefined organism found in <213> in SEQ ID (128) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (151)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (151)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (157) POS (112)
W 213	Artificial or Unknown found in <213> in SEQ ID (395)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (395)
W 213	Artificial or Unknown found in <213> in SEQ ID (396)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (396)
W 213	Artificial or Unknown found in <213> in SEQ ID (397)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (397)

**Input Set:**

**Output Set:**

**Started:** 2009-01-28 11:51:44.120  
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**Total Warnings:** 94  
**Total Errors:** 498  
**No. of SeqIDs Defined:** 401  
**Actual SeqID Count:** 401

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (398)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (398)
W 213	Artificial or Unknown found in <213> in SEQ ID (399)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (399)
W 213	Artificial or Unknown found in <213> in SEQ ID (400)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (400)



# SEQUENCE LISTING

<110> Plesch, Gunnar  
 Puzio, Piotr  
 Blau, Astrid  
 Looser, Ralf  
 Wendel, Birgit  
 Kamlage, Beate  
 Chardonnens, Agnes  
 Shirley, Amber  
 Wang, Xi-Qing  
 Sarria-Millan, Rodrigo  
 McKersie, Bryan  
 Chen, Ruoying

<120> PROCESS FOR THE PRODUCTION OF FINE CHEMICALS

<130> 12810-00197-US

<140> 10566644  
 <141> 2006-02-22

<150> EP 03016672.2  
 <151> 2003-08-01

<150> PCT/US2004/11887  
 <151> 2004-04-15

<160> 401

<170> PatentIn version 3.3

<210> 1  
 <211> 579  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)..(579)

<400> 1

atg tct gaa aag gcc gtt aga agg aaa ctt gtt att att ggt gat ggt	48
Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly Asp Gly	
1 5 10 15	
gct tgt ggc aag acc tct tta cta tat gta ttt aca tta gga aaa ttc	96
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Lys Phe	
20 25 30	
cct gaa caa tat cat ccg aca gtg ttc gag aat tat gtc act gat tgc	144
Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp Cys	
35 40 45	
aga gtt gac gga ata aaa gtg tcc tta acg ctc tgg gat aca gcg gga	192

Arg	Val	Asp	Gly	Ile	Lys	Val	Ser	Leu	Thr	Leu	Trp	Asp	Thr	Ala	Gly		
50						55				60							
caa	gag	gaa	tat	gaa	cgt	tta	cgt	cca	ttc	tca	tat	tca	aaa	gca	gat	240	
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Phe	Ser	Tyr	Ser	Lys	Ala	Asp		
65					70				75						80		
ata	ata	tta	att	ggg	ttt	gct	gta	gac	aat	ttt	gaa	tca	cta	att	aac	288	
Ile	Ile	Leu	Ile	Gly	Phe	Ala	Val	Asp	Asn	Phe	Glu	Ser	Leu	Ile	Asn		
					85				90						95		
gca	agg	acg	aaa	tgg	gcg	gat	gag	gca	tta	cga	tat	tgt	cct	gac	gca	336	
Ala	Arg	Thr	Lys	Trp	Ala	Asp	Glu	Ala	Leu	Arg	Tyr	Cys	Pro	Asp	Ala		
					100				105						110		
cca	atc	gtt	ctt	gta	ggc	ttg	aaa	aaa	gat	ttg	agg	caa	gaa	gcc	cat	384	
Pro	Ile	Val	Leu	Val	Gly	Leu	Lys	Lys	Asp	Leu	Arg	Gln	Glu	Ala	His		
					115				120						125		
ttt	aaa	gag	aat	gct	acc	gat	gaa	atg	gtt	ccc	att	gaa	gat	gca	aaa	432	
Phe	Lys	Glu	Asn	Ala	Thr	Asp	Glu	Met	Val	Pro	Ile	Glu	Asp	Ala	Lys		
130					135				140								
caa	gtt	gca	agg	gcc	att	ggg	gcc	aag	aaa	tac	atg	gaa	tgt	agt	gca	480	
Gln	Val	Ala	Arg	Ala	Ile	Gly	Ala	Lys	Lys	Tyr	Met	Glu	Cys	Ser	Ala		
145					150				155						160		
ctg	act	ggg	gag	ggg	gtg	gat	gat	gtc	ttt	gaa	gta	gct	aca	aga	acc	528	
Leu	Thr	Gly	Glu	Gly	Val	Asp	Asp	Val	Phe	Glu	Val	Ala	Thr	Arg	Thr		
					165				170						175		
agt	ttg	ctt	atg	aag	aag	gaa	cca	ggg	gct	aac	tgt	tgc	ata	att	tta	576	
Ser	Leu	Leu	Met	Lys	Lys	Glu	Pro	Gly	Ala	Asn	Cys	Cys	Ile	Ile	Leu		
					180				185						190		
taa																579	

Met	Ser	Glu	Lys	Ala	Val	Arg	Arg	Lys	Leu	Val	Ile	Ile	Gly	Asp	Gly
1				5					10					15	
Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Tyr	Val	Phe	Thr	Leu	Gly	Lys	Phe
			20					25					30		
Pro	Glu	Gln	Tyr	His	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Thr	Asp	Cys
		35					40					45			

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr Ala Gly  
50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys Ala Asp  
65 70 75 80

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu Ile Asn  
85 90 95

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro Asp Ala  
100 105 110

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu Ala His  
115 120 125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp Ala Lys  
130 135 140

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala  
145 150 155 160

Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr  
165 170 175

Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile Ile Leu  
180 185 190

<210> 3  
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<212> DNA  
<213> Oryza sativa

<220>  
<221> CDS  
<222> (1)..(600)

<400> 3  
atg ggt tgc tcc tcc tcc gtg cca gct cga agc act gga ggg ttg aac 48  
Met Gly Cys Ser Ser Ser Val Pro Ala Arg Ser Thr Gly Gly Leu Asn  
1 5 10 15

aat att agc aac gat aac tcc gct act gat tca aag gac ttg cgt gct 96  
Asn Ile Ser Asn Asp Asn Ser Ala Thr Asp Ser Lys Asp Leu Arg Ala  
20 25 30

aag ttg gta ttg ctt ggt gac tct ggt gta ggg aaa agt tgc att gtt 144  
Lys Leu Val Leu Leu Gly Asp Ser Gly Val Gly Lys Ser Cys Ile Val  
35 40 45

ctt cgc ttt gtt cgt ggt cag ttt gat ccc act tcc aag gta act gtc	192
Leu Arg Phe Val Arg Gly Gln Phe Asp Pro Thr Ser Lys Val Thr Val	
50 55 60	

ggg gca tca ttt tta tca caa aca ttg gct ttg gag gac tca aca ata	240
Gly Ala Ser Phe Leu Ser Gln Thr Leu Ala Leu Glu Asp Ser Thr Ile	
65 70 75 80	

gtg aaa ttt gaa ata tgg gat acc gct gga caa gag agg tat gct gcc	288
Val Lys Phe Glu Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Ala Ala	
85 90 95	

ttg gca cct ctt tac tac aga gga gct gct gct gca gtt gtt gtc tac	336
Leu Ala Pro Leu Tyr Tyr Arg Gly Ala Ala Ala Val Val Val Tyr	
100 105 110	

gac ata act agt cca gaa tca ttt agc aaa gca caa tac tgg gtg aag	384
Asp Ile Thr Ser Pro Glu Ser Phe Ser Lys Ala Gln Tyr Trp Val Lys	
115 120 125	

gaa ctt caa aaa cat ggt agt cct gat att atc atg gtt ttg gtt ggt	432
Glu Leu Gln Lys His Gly Ser Pro Asp Ile Ile Met Val Leu Val Gly	
130 135 140	

aat aaa gct gat cta cat gaa aat cga cat gta tct tct cag gaa gca	480
Asn Lys Ala Asp Leu His Glu Asn Arg His Val Ser Ser Gln Glu Ala	
145 150 155 160	

caa gag tat gca gag aag aat aat atg gtt ttc atc gag aca tca gca	528
Gln Glu Tyr Ala Glu Lys Asn Asn Met Val Phe Ile Glu Thr Ser Ala	
165 170 175	

aag aca gct gat aat ata aac caa gta ttt gag gaa att gcg aag agg	576
Lys Thr Ala Asp Asn Ile Asn Gln Val Phe Glu Glu Ile Ala Lys Arg	
180 185 190	

ttg ccc agg cca acg gcg tct tga	600
Leu Pro Arg Pro Thr Ala Ser	
195	

<210> 4  
 <211> 199  
 <212> PRT  
 <213> Oryza sativa

<400> 4

Met Gly Cys Ser Ser Ser Val Pro Ala Arg Ser Thr Gly Gly Leu Asn
1 5 10 15

Asn Ile Ser Asn Asp Asn Ser Ala Thr Asp Ser Lys Asp Leu Arg Ala
20 25 30

Lys Leu Val Leu Leu Gly Asp Ser Gly Val Gly Lys Ser Cys Ile Val  
35 40 45

Leu Arg Phe Val Arg Gly Gln Phe Asp Pro Thr Ser Lys Val Thr Val  
50 55 60

Gly Ala Ser Phe Leu Ser Gln Thr Leu Ala Leu Glu Asp Ser Thr Ile  
65 70 75 80

Val Lys Phe Glu Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Ala Ala  
85 90 95

Leu Ala Pro Leu Tyr Tyr Arg Gly Ala Ala Ala Ala Val Val Val Tyr  
100 105 110

Asp Ile Thr Ser Pro Glu Ser Phe Ser Lys Ala Gln Tyr Trp Val Lys  
115 120 125

Glu Leu Gln Lys His Gly Ser Pro Asp Ile Ile Met Val Leu Val Gly  
130 135 140

Asn Lys Ala Asp Leu His Glu Asn Arg His Val Ser Ser Gln Glu Ala  
145 150 155 160

Gln Glu Tyr Ala Glu Lys Asn Asn Met Val Phe Ile Glu Thr Ser Ala  
165 170 175

Lys Thr Ala Asp Asn Ile Asn Gln Val Phe Glu Glu Ile Ala Lys Arg  
180 185 190

Leu Pro Arg Pro Thr Ala Ser  
195

<210> 5

<211> 648

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(648)

<400> 5

atg gcg tcc agc gcg tcg cgg ttc atc aag tgc gtc acg gtc ggg gac

Met	Ala	Ser	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
1				5					10					15		
ggc	gcc	gtc	ggc	aag	acc	tgc	atg	ctc	atc	tgc	tac	acc	agc	aac	aag	96
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys	
			20					25					30			
ttc	ccc	act	gat	tac	gta	ccc	act	gtt	ttt	gac	aat	ttc	agt	gca	aac	144
Phe	Pro	Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
		35					40					45				
gtg	gtg	gtc	gac	ggc	acc	acg	gtg	aat	ttg	ggc	ctc	tgg	gat	act	gca	192
Val	Val	Val	Asp	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
	50					55				60						
ggg	cag	gaa	gat	tac	aac	aga	ttg	agg	ccg	cta	agc	tac	cgt	ggc	gcc	240
Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
65					70				75					80		
gat	gtc	ttt	gtg	ctt	gcc	ttc	tcc	cta	gtg	agc	cga	gct	agc	tat	gag	288
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser	Tyr	Glu	
			85					90					95			
aat	gtc	atg	aag	aag	tgg	tta	cca	gag	ctt	cag	cat	tat	gca	cca	ggg	336
Asn	Val	Met	Lys	Lys	Trp	Leu	Pro	Glu	Leu	Gln	His	Tyr	Ala	Pro	Gly	
			100					105					110			
gtg	cca	att	gtg	ttg	gtt	ggg	acc	aaa	ttg	gat	ctt	cgt	gaa	gat	aaa	384
Val	Pro	Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys	
		115				120						125				
cac	tac	tta	ctt	gac	cat	cct	agc	ttg	gtg	cct	gtg	act	aca	gca	cag	432
His	Tyr	Leu	Leu	Asp	His	Pro	Ser	Leu	Val	Pro	Val	Thr	Thr	Ala	Gln	
	130					135				140						
gga	gag	gaa	ctc	cgc	aag	cac	att	ggc	gca	acg	tgt	tac	atc	gaa	tgc	480
Gly	Glu	Glu	Leu	Arg	Lys	His	Ile	Gly	Ala	Thr	Cys	Tyr	Ile	Glu	Cys	
145					150				155					160		
agc	tca	aag	aca	cag	cag	aat	gta	aaa	gct	gtg	ttt	gat	gct	gcc	atc	528
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
			165					170					175			
aag	gta	gta	atc	aag	cct	cca	aca	aag	cag	agg	gac	agg	aag	aag	aag	576
Lys	Val	Val	Ile	Lys	Pro	Pro	Thr	Lys	Gln	Arg	Asp	Arg	Lys	Lys	Lys	
			180					185					190			
aaa	aca	cgg	cgc	gga	tgt	tct	ttc	ttc	tgc	aag	ggc	gtc	atg	tcc	aga	624
Lys	Thr	Arg	Arg	Gly	Cys	Ser	Phe	Phe	Cys	Lys	Gly	Val	Met	Ser	Arg	
		195				200						205				
aga	agg	cta	gta	tgc	ttc	aag	tga									648
Arg	Arg	Leu	Val	Cys	Phe	Lys										

<210> 6  
<211> 215  
<212> PRT  
<213> Oryza sativa

<400> 6

Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp  
1 5 10 15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys  
20 25 30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn  
35 40 45

Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp Thr Ala  
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala  
65 70 75 80

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser Tyr Glu  
85 90 95

Asn Val Met Lys Lys Trp Leu Pro Glu Leu Gln His Tyr Ala Pro Gly  
100 105 110

Val Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys  
115 120 125

His Tyr Leu Leu Asp His Pro Ser Leu Val Pro Val Thr Thr Ala Gln  
130 135 140

Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Cys Tyr Ile Glu Cys  
145 150 155 160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile  
165 170 175

Lys Val Val Ile Lys Pro Pro Thr Lys Gln Arg Asp Arg Lys Lys Lys  
180 185 190

<400>	7																
atg agc gca tcg agg ttc ata aag tgt gtt aca gtc ggc gat ggt gcc																	48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp Gly Ala																	
1	5				10						15						
gtc gga aaa acc tgt atg ctg atc tct tac acc agc aac act ttc cct																	96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr Phe Pro																	
	20				25						30						
acg gac tat gtt cca act gtt ttc gac aac ttc agt gct aac gtg gtt																	144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn Val Val																	
	35				40						45						
gtt gat ggg aac act gtg aat ctt gga ttg tgg gat aca gct ggt caa																	192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln																	
	50				55						60						
gaa gac tat aac agg tta aga cca ttg agt tac cgt ggt gca gat gtc																	240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val																	
65	70				75						80						
ttc att ctt gct ttc tct ctt att agc aaa gct agc tac gag aac ata																	288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu Asn Ile																	
	85				90						95						
gcc aag aag tgg att cct gag ctc agg cat tat gcc cct gga gtt cct																	336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly Val Pro																	
	100				105						110						
atc att ctc gtg ggg aca aaa ctc gat ctt cga gat gac aag cag ttc																	384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Gln Phe																	
	115				120						125						
ttc ata gac cat ccc ggt gca gtg cca atc act aca aac cag gga gag																	432
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln Gly Glu																	
	130				135						140						
gaa cta aag aaa ctc ata gga tct cca gtt tac att gaa tgt agt tca																	480
Glu Leu Lys Lys Leu Ile Gly Ser Pro Val Tyr Ile Glu Cys Ser Ser																	



145	150	155	160	
aag acg cag cag aat gtc aaa gca gtc ttt gac gca gct att aaa gtg				528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile Lys Val				
	165	170	175	
gtg ctt cag cca cca aaa tca aag aag aag aaa aag aac aag aat cgt				576
Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Lys Lys Asn Lys Asn Arg				
	180	185	190	
tgc gtt ttc ttg tga				